GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 5, 2005, 11:07:01 ; Search time 156 Seconds
(without alignments)
45.991 Million cell updates/sec

Title: US-10-827-083-4
Perfect score: 105
Sequence: 1 CDSTLRLCVQSTHVDIRTLE 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	105	100.0	20	5	AAU10804	Aau10804 Human pap
2	105	100.0	30	2	AAR15575	Aar15575 Immunopep
3	105	100.0	30	2	AAW93290	Aaw93290 Human pap
4	105	100.0	50	6	AAO16632	Aao16632 Human pap
5	105	100.0	92	7	ADF74305	Adf74305 Human pap
6	105	100.0	98	2	AAR22767	Aar22767 HPV E7 pe
7	105	100.0	98	2	AAR42361	Aar42361 Human pap
8	105	100.0	98	2	AAW46886	Aaw46886 Amino aci
9	105	100.0	98	2	AAY08020	Aay08020 Human pap
10	105	100.0	98	3	AAY58474	Aay58474 Human pap
11	105	100.0	98	3	AAY50703	Aay50703 HPV16 E7
12	105	100.0	98	3	AAY57721	Aay57721 Human pap
13	105	100.0	98	4	AAB98421	Aab98421 Human pap
14	105	100.0	98	4	AAU01718	Aau01718 Human pap
15	105	100.0	98	4	AAU72607	Aau72607 Human pap
16	105	100.0	98	4	AAB67546	Aab67546 Amino aci
17	105	100.0	98	4	AAB49453	Aab49453 HPV 16E7.
18	105	100.0	98	4	AAB31607	Aab31607 Amino aci
19	105	100.0	98	4	AAB86332	Aab86332 HPV 16 E7
20	105	100.0	98	5	AAU77713	Aau77713 Human pap
21	105	100.0	98	5	AAU10810	Aau10810 Human pap
22	105	100.0	98	5	ABB82375	Abb82375 Wild-type
23	105	100.0	98	6	AAO22639	Aao22639 HPV-16 pr
24	105	100.0	98	6	AAO16630	Aao16630 Human pap
25	105	100.0	98	7	ADF09516	Adf09516 Human pap
26	105	100.0	98	7	ADF18635	Adf18635 Human pap
27	105	100.0	98	7	ADF18632	Adf18632 Human pap
28	105	100.0	98	8	ADL90076	Adl90076 Human pap
29	105	100.0	98	8	ADM32916	Adm32916 Amino aci
30	105	100.0	98	8	ADO44073	Ado44073 Amino aci
31	105	100.0	98	8	ADN49005	Adn49005 Human pap
32	105	100.0	99	5	ABB81111	Abb81111 HPV E7 an
33	105	100.0	99	5	ABB82376	Abb82376 Modified
34	105	100.0	99	7	ADE21865	Ade21865 HPV-16 E7
35	105	100.0	99	8	ADO05276	Ado05276 Human pap
36	105	100.0	99	8	ADQ88451	Adq88451 HPV16 E7
37	105	100.0	111	5	AAO22923	Aao22923 Human pap
38	105	100.0	121	4	AAB31608	Aab31608 Amino aci
39	105	100.0	172	2	AAR97563	Aar97563 Human pap
40	105	100.0	185	2	AAW99370	Aaw99370 Papilloma
41	105	100.0	198	4	AAB31616	Aab31616 Amino aci
42	105	100.0	220	2	AAY25375	Aay25375 HPV fusio
43	105	100.0	220	2	AAY25378	Aay25378 HPV fusio
44	105	100.0	220	2	AAY02631	Aay02631 ProtDthr1
45	105	100.0	220	2	AAY02634	Aay02634 Prot.D1/3

ALIGNMENTS

RESULT 1
AAU10804
ID AAU10804 standard; peptide; 20 AA.
XX
AC AAU10804;
XX
DT 29-AUG-2003 (revised)
DT 14-FEB-2002 (first entry)
XX
DE Human papillomavirus (HPV) 16 E7 coding region derived peptide #2.
XX
KW Human papillomavirus 16; HPV 16; cancer; squamous cell carcinoma;
KW adenocarcinoma; koilocytosis; hyperkerotosis; intraepithelial neoplasia;
KW intraepithelial lesion; dysplasia; head cancer; neck cancer;
KW small cell lung cancer; melanoma; oncogene.
XX
OS Human papillomavirus type 16.
XX
PN WO200177142-A1.
XX
PD 18-OCT-2001.
XX
PF 05-APR-2001; 2001WO-US011233.
XX
PR 05-APR-2000; 2000US-0194796P.
XX
PA (IMPA-) IMPACT DIAGNOSTICS INC.
XX
PI Hu YX;
XX
DR WPI; 2002-010888/01.
XX
PT New peptides derived from E2, E6 or E7 early coding regions of human
PT papillomavirus 16 and 18, useful in diagnosis of human papillomavirus
PT infection and associated malignancy e.g. cervical carcinoma.
XX
PS Claim 2; Fig 3; 28pp; English.
XX
CC The invention describes a novel peptide derived from the E2, E6 or E7
CC early coding region of human papillomavirus (HPV) 16 and 18, which is
CC soluble in aqueous solution and has a lysine or cysteine residue near the
CC amino terminus, very few tryptophan, methionine and cysteine residues,
CC and/or many glycine and asparagine residues. The peptides and diagnostic
CC method are used to diagnose HPV infection, especially infection with
CC oncogenic HPV by using peptides derived from the E2 region, since HPV 16
CC and 18 are the main HPV genetic types associated with cancers, and
CC presence of antibodies to E2 protein is known to provide evidence of HPV
CC infection. They are also useful to diagnose HPV associated malignancy or

CC premalignancy, especially carcinoma by using peptides derived from the E6
CC or E7 regions, since E6 and E7 are thought to be tumour-specific
CC antigens. The peptides and diagnostic method are especially useful to
CC diagnose cervical carcinoma (e.g. adenocarcinoma of the uterine cervix)
CC and any HPV associated epithelial cell abnormality including high grade
CC dysplasias, koilocytosis, hyperkerotosis, precancerous conditions
CC encompassing intraepithelial neoplasias or intraepithelial lesions, and
CC invasive or malignant cancers. They are also used to detect head and neck
CC cancers, small cell lung cancers, penal and anal squamous cell carcinomas
CC and melanoma. This is the amino acid sequence of peptide epitope #2,
CC derived from the E7 early coding region of HPV 16, an oncoprotein that
CC destabilises cell cycle control through its interaction with the cyclin-
CC dependent kinase inhibitor protein, p21, described in the method of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 105; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRLCVQSTHVDIRTLE 20
||||||||||||||||||||
Db 1 CDSTLRLCVQSTHVDIRTLE 20

RESULT 2
AAR15575
ID AAR15575 standard; protein; 30 AA.
XX
AC AAR15575;
XX
DT 02-MAR-1992 (first entry)
XX
DE Immunopeptide #8 derived from HPV16 E7 peptide.
XX
KW cervical cancer; cervical intraepithelial neoplasia; CIN; wart;
KW squamous cell carcinoma; ELISA; HPV 16.
XX
OS Synthetic.
XX
PN WO9118294-A.
XX
PD 28-NOV-1991.
XX
PF 11-MAY-1990; 90SE-00001705.
XX
PR 11-MAY-1990; 90SE-00001705.
XX
PA (MEDS-) MEDSCAND AB.
XX
PI Dillner J, Dillner L, Cheng HM;
XX
DR WPI; 1991-369390/50.
XX
PT Diagnosis of human papilloma virus infection and PV-carrying tumours -
PT using synthetic peptide(s) to detect virus specific antigen-antibody
PT complexes by immunoassay.
XX
PS Disclosure; Page 38; 72pp; English.
XX
CC This is one of two peptides which have been synthesised on the basis of
CC the amino acid sequence for the E7 protein of HPV 16. The selection of
CC peptide sequences was based on the assumption that an immunoreactive
CC region might be situated in the same relative region of a protein from
CC different HPV types. The peptides were used in diagnostic immunoassays to
CC detect HPV-infection. See AAR15523-R15601
XX
SQ Sequence 30 AA;

Query Match 100.0%; Score 105; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRLCVQSTHVDIRTLE 20
||||||||||||||||||||
Db 4 CDSTLRLCVQSTHVDIRTLE 23

RESULT 3
AAW93290
ID AAW93290 standard; peptide; 30 AA.
XX
AC AAW93290;
XX
DT 27-MAY-1999 (first entry)
XX
DE Human papillomavirus peptide fragment #4.
XX
KW Diagnosis; skin; immune reaction; onco-protein; E6; E7.
XX
OS Human papillomavirus.
XX
PN DE19737409-A1.
XX
PD 04-MAR-1999.
XX
PF 27-AUG-1997; 97DE-01037409.
XX
PR 27-AUG-1997; 97DE-01037409.
XX
PA (MEDI-) MEDIGENE AG.
XX
PI Hoepfl R;
XX
DR WPI; 1999-168276/15.
XX
PT Diagnosis kit for testing skin for immune reactions against onco-protein
PT E6 and E7 - comprises onco-protein E6 and E7 and/or immunologically
PT active parts of E6 and E7 derived from human papilloma virus.
XX
PS Disclosure; Col 3; 4pp; German.
XX
CC This invention describes peptides used in a diagnosis kit for testing
CC skin for immune reactions against onco-protein E6 and E7. The method of
CC the invention comprises onco-protein E6 and E7 and/or immunologically
CC active parts of E6 and E7 derived from human papilloma virus
XX
SQ Sequence 30 AA;

Query Match 100.0%; Score 105; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 9.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRLCVQSTHVDIRTLE 20
||||||||||||||||||||
Db 1 CDSTLRLCVQSTHVDIRTLE 20

RESULT 4
AAO16632
ID AAO16632 standard; peptide; 50 AA.
XX
AC AAO16632;
XX
DT 15-MAY-2003 (first entry)
XX
DE Human papillomavirus E7 antigen-related peptide #2.
XX
KW Epitope; E7 antigen; CD4-positive T cell activation;
KW uterine cancer lesion.
XX
OS Unidentified.
XX
PN WO2002100889-A1.
XX

PD 19-DEC-2002.
XX
PF 10-JUN-2002; 2002WO-JP005747.
XX
PR 08-JUN-2001; 2001JP-00173803.
XX
PA (KIRI) KIRIN BEER KK.
XX
PI Maeda H, Okubo M;
XX
DR WPI; 2003-156946/15.
XX
PT Novel epitope of human papilloma virus E7 antigen capable of activating
PT CD4-positive T cells specific to (pre-)uterine cancer lesion, applicable
PT in drug compositions for preventing and treating uterine cancer.
XX
PS Example 4; Page 16; 40pp; Japanese.
XX
CC The invention comprises an epitope of the human papillomavirus E7 antigen
CC that is capable of activating CD4-positive T cells that are specific to
CC uterine cancer lesions. The epitope of the invention is useful for
CC preventing and treating uterine cancer. The present amino acid sequence
CC represents a peptide that was used in an example of the invention
XX
SQ Sequence 50 AA;

Query Match 100.0%; Score 105; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRLCVQSTHVDIRTLE 20
||||||||||||||||||||
Db 13 CDSTLRLCVQSTHVDIRTLE 32

RESULT 5
ADF74305
ID ADF74305 standard; protein; 92 AA.
XX
AC ADF74305;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human papillomavirus-16 (HPV-16) E7 delta21-26 mutant protein.
XX
KW mutein; human papillomavirus-16; HPV-16; E7; HPV-16 E7 delta21-26;
KW mutant; humoral; cellular response; immunosuppressive; vaccine; cancer;
KW tumour development.
XX
OS Synthetic.
OS Human papillomavirus type 16.
XX
PN WO2003090664-A2.
XX
PD 06-NOV-2003.
XX
PF 24-APR-2003; 2003WO-BE000073.
XX
PR 24-APR-2002; 2002FR-00005173.
PR 13-SEP-2002; 2002US-0410461P.
PR 03-APR-2003; 2003FR-00004170.
XX
PA (ULBR) UNIV LIBRE BRUXELLES.
XX
PI Hallez S, Burny A, Jacquet A, Bollen A;
XX
DR WPI; 2003-865511/80.
DR N-PSDB; ADF74304.
XX
PT New mutated human papillomavirus-16 E7 polypeptide having a deleted
PT sequence from amino acid 21 to 26, useful for manufacturing a medicament
PT in the treatment or prevention of cancer, preferably cancer induced by a
PT human papillomavirus.
XX
PS Claim 1; SEQ ID NO 2; 39pp; English.
XX
CC This invention relates to a novel mutated human papillomavirus-16 (HPV-
CC 16) E7 polypeptide and the pharmaceutical compositions derived thereof.
CC Specifically, it refers to the HPV-16 E7 delta21-26 mutant (residues 21-
CC 26 have been deleted), which induces a specific humoral and cellular
CC response against infectious agents, and furthermore can reduce or block
CC the immunosuppressive characteristics of the native HPV-16 E7 protein.
CC The present invention also describes a fusion protein consisting of HPV-
CC 16 E7 delta21-26 with an HIV tat polypeptide, and inhibitors directed
CC against these proteins such as antibodies, antisense RNA oligos or
CC ribozymes that can block expression. Accordingly, various pharmaceutical
CC compositions or vaccines can be derived that are useful for the
CC manufacture of a medicament for the treatment and/ or prevention of
CC cancer and tumour development, preferably a cancer induced by a human
CC papillomavirus, especially the strain of HPV-16. This polypeptide
CC sequence is the recombinant HPV-16 E7 delta21-26 mutant protein of the
CC invention.
XX
SQ Sequence 92 AA;

Query Match 100.0%; Score 105; DB 7; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRLCVQSTHVDIRTLE 20
||||||||||||||||||||
Db 55 CDSTLRLCVQSTHVDIRTLE 74

RESULT 6
AAR22767
ID AAR22767 standard; peptide; 98 AA.
XX
AC AAR22767;
XX
DT 25-MAR-2003 (revised)
DT 21-SEP-1992 (first entry)
XX
DE HPV E7 peptide.
XX
KW Human; papillomavirus; immunogenic; cervical; warts; carcinoma; cancer.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9205248-A.
XX
PD 02-APR-1992.
XX
PF 26-SEP-1991; 91WO-US007081.
XX
PR 26-SEP-1990; 90US-00588384.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Thomas EK, Chen L, Blake J, Hellstrom K, Hellstrom I, Hu SL;
XX
DR WPI; 1992-132119/16.
XX
PT Immunogenic peptide(s) derived from E6 or E7 region of HPV16 - and
PT recombinant cells encoding them, useful in treatment and prophylaxis of
PT cervical warts or cancer resulting from HPV infection.
XX
PS Disclosure; Fig 7; 81pp; English.
XX
CC The peptide is the sequence of the human papillomavirus HPV 16 E7
CC nucleoprotein. Peptides corresponding to regions (pref. epitopic regions)
CC of HPV 16 E7 were synthesised by standard Merrifield synthesis. Examples
CC of such peptides are E7 1-10, 29-50 or 70-81. Compositions contg. these
CC peptides, antibodies against the peptides, or recombinant cells contg.
CC the gene encoding the immunogenic peptides may be utilised in methods for

```
CC   inhibiting and treating HPV infection and tumour initiation and
CC   progression e.g. in the prevention or retardation of cervical warts and
CC   cervical carcinoma resulting from HPV infection. See also AAR22766.
CC   (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
CC   correct PI field.)
XX
SQ   Sequence 98 AA;

  Query Match             100.0%;  Score 105;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 7
AAR42361
ID   AAR42361 standard; protein; 98 AA.
XX
AC   AAR42361;
XX
DT   25-MAR-2003  (revised)
DT   21-MAY-1994  (first entry)
XX
DE   Human papillomavirus 16 E7 protein and fragments.
XX
KW   Tumours; cows; horses; donkeys; regression; udder warts; HPV16.
XX
OS   Synthetic.
XX
PN   WO9320844-A1.
XX
PD   28-OCT-1993.
XX
PF   01-APR-1993;   93WO-GB000679.
XX
PR   08-APR-1992;   92GB-00007701.
XX
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Camp MS;
XX
DR   WPI; 1993-351368/44.
XX
PT   Use of papilloma-virus E7 protein or fragments for the therapy of
PT   papilloma-virus disease - for the regression of tumours e.g. removal of
PT   warts from udders or mouth of milking cows or for treatment of horses or
PT   donkeys.
XX
PS   Disclosure; Fig 2; 31pp; English.
XX
CC   The sequence is that of the human papillomavirus type 16 E7 protein. The
CC   protein sequence was aligned with that of bovine papillomavirus type 4.
CC   See also AAR42360. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 98 AA;

  Query Match             100.0%;  Score 105;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 8
AAW46886
ID   AAW46886 standard; protein; 98 AA.
XX
AC   AAW46886;
XX
DT   25-MAR-2003  (revised)
DT   15-JUN-1998  (first entry)
XX
DE   Amino acid sequence of the HPV-16 E7 oncoprotein.
XX
KW   E7 oncoprotein; proliferative state; HPV; kinase activity;
KW   cyclin/cyclin-dependent kinase; p21CIP1; interaction; inactivation;
KW   cyclin/cyclin-dependent kinase inhibitor.
XX
OS   Human papillomavirus.
XX
PN   US5736318-A.
XX
PD   07-APR-1998.
XX
PF   17-MAR-1995;   95US-00406248.
XX
PR   17-MAR-1995;   95US-00406248.
XX
PA   (HARD ) UNIV HARVARD.
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Muenger K,  Jones DL;
XX
DR   WPI; 1998-239202/21.
DR   N-PSDB; AAV16717.
XX
PT   Evaluation of proliferative state of cells transformed with human
PT   papilloma virus - by determining cyclin-dependent kinase activity induced
PT   by E7 onco-protein.
XX
PS   Disclosure; Col 19-20; 14pp; English.
XX
CC   The present sequence represents Human papillomavirus (HPV), strain 16, E7
CC   oncoprotein. The proliferative state of a cell transformed with HPV can
CC   be evaluated in the following manner. Cyclin/cyclin-dependent kinase
CC   complexes containing protein p21CIP1 (AAW46887-88) are isolated from the
CC   transformed cell, and the HPV E7 oncoprotein added to the isolated
CC   protein. Cyclin/cyclin-dependent kinase complexes are isolated from an
CC   untransformed cell that is substantially homogenic with the transformed
CC   cell, and the HPV E7 oncoprotein added. The kinase activities of the 2
CC   samples are measured, where a proliferating transformed cell has a
CC   greater kinase activity that the untransformed cell. The method is used
CC   for determining the extent of interaction and/or inactivation between a
CC   cyclin/cyclin-dependent kinase inhibitor and the HPV E7 oncoprotein and
CC   thus evaluating the proliferative state of a transformed cell. (Updated
CC   on 25-MAR-2003 to correct PI field.)
XX
SQ   Sequence 98 AA;

  Query Match             100.0%;  Score 105;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 9
AAY08020
ID   AAY08020 standard; protein; 98 AA.
XX
AC   AAY08020;
XX
DT   27-AUG-2003  (revised)
DT   08-JUL-1999  (first entry)
XX
DE   Human papilloma virus E7 protein.
XX
KW   L1 protein; capsomer; virus; vaccine; infection; treatment; prevention;
KW   cervical carcinoma; fusion protein; anti-capsid; antibody; E7 protein;
```

KW antigenicity.
XX
OS Human papillomavirus.
XX
PN WO9918220-A1.
XX
PD 15-APR-1999.
XX
PF 06-OCT-1998; 98WO-US020965.
XX
PR 06-OCT-1997; 97US-00944368.
XX
PA (LOYO) UNIV LOYOLA CHICAGO.
XX
PI Gissmann L, Mueller M;
XX
DR WPI; 1999-264026/22.
DR N-PSDB; AAX37567.
XX
PT Human papilloma virus (HPV) L1 fusion protein capsomers, used in vaccines
PT against HPV infection.
XX
PS Disclosure; Page 33; 48pp; English.
XX
CC This invention describes novel vaccines comprising a human papilloma
CC virus (HPV) capsomer, composed of a HPV L1 fusion protein or a HPV L1
CC truncated protein. The vaccines can prevent or treat human papilloma
CC virus infection. Such therapeutic vaccinations can be used for relief
CC against, e.g. cervical carcinoma. Construction of chimeric proteins
CC comprising amino acid residues from L1 protein, and e.g. E6 or E7
CC protein, which give rise to chimeric capsomers, combines prophylactic and
CC therapeutic functions of a vaccine. Capsomers can promote elimination of
CC persistently infected cells. Capsomers can also escape neutralization by
CC pre-existing anti-capsid antibodies and hence possess longer circulating
CC half-life as compared to chimeric virus-like particles. The fusion
CC protein, which forms the capsomer, provides increased antigenicity.
CC (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 98 AA;

Query Match 100.0%; Score 105; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRLCVQSTHVDIRTLE 20
||||||||||||||||||||
Db 61 CDSTLRLCVQSTHVDIRTLE 80

RESULT 10
AAY58474
ID AAY58474 standard; protein; 98 AA.
XX
AC AAY58474;
XX
DT 10-APR-2000 (first entry)
XX
DE Human papillomavirus (HPV) E7 oncoprotein.
XX
KW HPV E7 oncoprotein; proteasome activity; degradation; virus component;
KW viral infection; inflammatory disease; anti-inflammatory; anti-HIV;
KW virucide.
XX
OS Human papillomavirus.
XX
PN WO9966065-A2.
XX
PD 23-DEC-1999.
XX
PF 10-JUN-1999; 99WO-GB001840.
XX
PR 13-JUN-1998; 98GB-00012756.
PR 13-JUN-1998; 98GB-00012757.
PR 13-JUN-1998; 98GB-00012758.
PR 13-JUN-1998; 98GB-00012759.
PR 13-JUN-1998; 98GB-00012760.
XX
PA (BRID-) BRIDGEHEAD TECHNOLOGIES LTD.
XX
PI Schmid H, Petit F, Kloetzel P, Jarrousse A, Gautier K, Badaoui S;
PI Mouzeyar S, Nicolas P;
XX
DR WPI; 2000-106109/09.
XX
PT Novel assay methods for identifying compounds which modulate and/or
PT regulate proteosomal activity.
XX
PS Disclosure; Page 8; 35pp; English.
XX
CC The invention relates to a novel assay for identifying compounds which
CC inhibit viral replication and pathogenesis by increasing proteasomal
CC degradation of viral components or molecules induced by viral infection.
CC The method comprises reacting a compound with proteasomal protein (20S
CC proteasomes separately with or without 19S and 11S complexes), viral gene
CC product, and protein or peptide substrates; measuring protease activity;
CC and identifying the compound as an inhibitor if the protease activity of
CC the assay system is increased. The assays of the invention can be used to
CC identify compounds which inhibit viral replication and pathogenesis, and
CC modulate and/or regulate proteasome activity. Compounds which increase
CC proteasomal degradation of viral components or molecules induced by viral
CC infection are of value in the treatment of viral disease. Compounds which
CC modulate proteasomal nuclease activity have use in the treatment of
CC inflammatory disease, and AIDS in HIV infected patients. The methods may
CC also be used to generate resistance to bacterial or viral damage.
CC Sequences AAY58472-Y58474 represent examples of viral proteins which
CC affect proteasomal function
XX
SQ Sequence 98 AA;

Query Match 100.0%; Score 105; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRLCVQSTHVDIRTLE 20
||||||||||||||||||||
Db 61 CDSTLRLCVQSTHVDIRTLE 80

RESULT 11
AAY50703
ID AAY50703 standard; protein; 98 AA.
XX
AC AAY50703;
XX
DT 04-FEB-2000 (first entry)
XX
DE HPV16 E7 protein.
XX
KW E7 protein; immunogenic; active immunization.
XX
OS Human papillomavirus.
XX
PN WO9955876-A2.
XX
PD 04-NOV-1999.
XX
PF 30-APR-1999; 99WO-DE001331.
XX
PR 30-APR-1998; 98DE-01019476.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Gissmann L, Jochmus I;
XX
DR WPI; 2000-023362/02.
DR N-PSDB; AAZ24129.

XX
PT Immunogenic protein with altered biological function, useful for active
PT immunization.
XX
PS Example 1; Page 25; 33pp; German.
XX
CC This invention describes the construction of a novel polypeptide with
CC immunogenic and altered biological function of a protein, where the
CC polypeptide has regions of the protein of about 10-40 amino acids in a
CC different order. The polypeptide, or its DNA, is useful for active
CC immunization without cross-reactivity and problems associated with the
CC biological function of the protein. This sequence represents the human
CC papillomavirus type 16 E7 protein which is used to illustrate the method
CC of the invention
XX
SQ Sequence 98 AA;

Query Match 100.0%; Score 105; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRLCVQSTHVDIRTLE 20
||||||||||||||||||||
Db 61 CDSTLRLCVQSTHVDIRTLE 80

RESULT 12
AAY57721
ID AAY57721 standard; protein; 98 AA.
XX
AC AAY57721;
XX
DT 14-MAR-2000 (first entry)
XX
DE Human papillomavirus 16 E7 protein SEQ ID NO:4.
XX
KW Human papillomavirus; HPV; L1 fusion protein; vaccine; cytostatic;
KW viral capsomere; virucide; dermatological; malignant tumour formation;
KW cervical cancer; cervical intraepithelial neoplasia; genital wart;
KW condylomata acuminata.
XX
OS Human papillomavirus.
XX
PN CA2229955-A1.
XX
PD 20-AUG-1999.
XX
PF 20-FEB-1998; 98CA-02229955.
XX
PR 20-FEB-1998; 98CA-02229955.
XX
PA (MEDI-) MEDIGENE GMBH.
XX
PI Burger A, Hallek M;
XX
DR WPI; 2000-063092/06.
DR N-PSDB; AAZ48175.
XX
PT Fusion proteins comprising papillomavirus specific proteins useful for
PT vaccinating against malignant tumors of the anogenital tract such as
PT cervical carcinomas.
XX
PS Example 1; Page 34; 46pp; English.
XX
CC The present invention describes a fusion protein comprising 2 amino acids
CC sequences from 2 different papillomavirus specific (PVS) proteins. The
CC fusion protein may be administered for preventing and treating
CC papillomavirus infections in humans and animals. Papillomaviruses are
CC implicated in the pathology of malignant tumour formation in the
CC anogenital tract (of these tumours, cervical cancer is the most frequent
CC (500000 cases/year) and in the formation of precursor lesions of cervical
CC intraepithelial neoplasia (CIN). Papillomaviruses also cause benign
CC genital warts such as condylomata acuminata. However, the type and
CC severity of disease caused by the papillomavirus is dependent on the
CC strain causing the infection. The present sequence represents the human
CC papillomavirus 16 E7 protein
XX
SQ Sequence 98 AA;

Query Match 100.0%; Score 105; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRLCVQSTHVDIRTLE 20
||||||||||||||||||||
Db 61 CDSTLRLCVQSTHVDIRTLE 80

RESULT 13
AAB98421
ID AAB98421 standard; protein; 98 AA.
XX
AC AAB98421;
XX
DT 22-AUG-2001 (first entry)
XX
DE Human papillomavirus protein HPV16 E7.
XX
KW Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;
KW epitope; T cell; identification; vaccine; infection; genital wart;
KW neoplastic growth; antiviral.
XX
OS Human papillomavirus.
XX
PN WO200141799-A1.
XX
PD 14-JUN-2001.
XX
PF 11-DEC-2000; 2000WO-US033549.
XX
PR 10-DEC-1999; 99US-0172705P.
PR 15-AUG-2000; 2000US-00641528.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;
XX
DR WPI; 2001-381497/40.
XX
PT An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT treating HPV infections.
XX
PS Disclosure; Page 21; 756pp; English.
XX
CC The present invention describes an isolated prepared human papillomavirus
CC (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine
CC production. Peptides and corresponding nucleic acid compositions from the
CC present invention are useful for stimulating an immune response to HPV by
CC stimulating the production of CTL or HTL responses, specifically in the
CC treatment or prophylaxis of HPV infection, in persons who have not
CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides
CC can also be used in a tetramer staining assay to assess peripheral blood
CC mononuclear cells for the presence of antigen-specific CTLs following
CC exposure to a pathogen or immunogen, and as reagents to evaluate immune
CC recall responses or evaluate the efficacy of a vaccine. The vaccine
CC compositions are useful for removing warts or treating HPV infections.
CC The epitopes for inclusion in an epitope-base vaccine may be selected
CC from conserved regions of viral or tumour-associated antigens, which
CC reduces the likelihood of escape mutants, also immunosuppressive epitopes
CC that may be present in whole antigens can be avoided with the use of
CC epitope-base vaccines. An additional advantage is the ability to combine
CC selected epitopes (CTL and HTL) and to modify the composition of the
CC epitopes achieving enhanced immunogenicity, the major benefit of the
CC vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent
CC polypeptide sequences used in the exemplification of the present
CC invention

```
XX
SQ   Sequence 98 AA;

  Query Match             100.0%;  Score 105;  DB 4;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 14
AAU01718
ID   AAU01718 standard; protein; 98 AA.
XX
AC   AAU01718;
XX
DT   29-AUG-2001  (first entry)
XX
DE   Human papilloma virus-16 (HPV-16) E7 antigen.
XX
KW   Mouse; granulocyte-macrophage-colony stimulating factor; GM-CSF;
KW   chimeric; heat shock protein; HSP; Flt-3 ligand; FL; exotoxin A; ETA dII;
KW   antigenic; immunogenic; cytotoxic T cell response; tumour; vaccine;
KW   immunotherapy; HPV-16; E7 antigen.
XX
OS   Human papillomavirus.
XX
PN   WO200129233-A2.
XX
PD   26-APR-2001.
XX
PF   20-OCT-2000; 2000WO-US041422.
XX
PR   20-OCT-1999;   99US-00421608.
PR   09-FEB-2000; 2000US-00501097.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI   Wu T,  Hung C;
XX
DR   WPI; 2001-290921/30.
DR   N-PSDB; AAS02608.
XX
PT   New chimeric polypeptide, useful as anti-tumor vaccines, comprises
PT   carboxy terminal fragment of heat shock protein, Flt-3 ligand or
PT   cytoplasmic translocation domain of Pseudomonas exotoxin A and antigenic
PT   polypeptide.
XX
PS   Example 1; Page 39; 110pp; English.
XX
CC   The sequence represents the amino acid sequence of human papilloma virus-
CC   16 (HPV-16) E7 antigen used in construction of a chimeric polypeptide
CC   comprising: (a) a first polypeptide domain containing a carboxy terminal
CC   fragment of a heat shock protein (HSP), an Flt-3 ligand (FL), a
CC   cytoplasmic translocation domain of a Pseudomonas exotoxin A (ETA dII),
CC   or a granulocyte-macrophage colony stimulating factor (GM-CSF); and (b) a
CC   second polypeptide domain containing an antigenic polypeptide. A
CC   composition comprising the chimeric polypeptide is useful for inducing an
CC   immune response such as a cytotoxic T cell response. The nucleic acid or
CC   vector encoding the chimeric polypeptide present in the composition is
CC   administered as naked DNA by gene gun or equivalent, or by liposomal
CC   formulation. These are thus useful for vaccinating a mammal against
CC   infection by inducing an immune response to a pathogen. Preferably they
CC   are useful for vaccinating a mammal against a tumour antigen. The
CC   compositions and methods are useful for stimulating or enhancing the
CC   immunogenicity of a selected antigen or stimulating or enhancing a
CC   cellular immune response specific for that antigen. The chimeric nucleic
CC   acid molecules and vaccination methods, yield potent antigen-specific
CC   immunotherapy. The polynucleotides and DNA vaccines can induce a cellular
CC   immune response that is at least 40 fold more potent than conventional
CC   DNA vaccines. The vaccines are safe and useful for administration to
CC   domesticated or agricultural animals, as well as humans, and have low
CC   immunogenicity
XX
SQ   Sequence 98 AA;

  Query Match             100.0%;  Score 105;  DB 4;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 15
AAU72607
ID   AAU72607 standard; protein; 98 AA.
XX
AC   AAU72607;
XX
DT   06-AUG-2003  (revised)
DT   26-FEB-2002  (first entry)
XX
DE   Human papilloma virus (HPV) E7 fragment.
XX
KW   Human papillomavirus; HPV; E7; cyclin E; cyclin A; virucide;
KW   E7-induced cyclin-dependent kinase-2; CDK2 kinase; HPV infection;
KW   adenoviral infection; simian virus 40 infection; SV40.
XX
OS   Human papillomavirus.
XX
PN   US2001029022-A1.
XX
PD   11-OCT-2001.
XX
PF   01-DEC-2000; 2000US-00728466.
XX
PR   25-AUG-1999;   99US-00382616.
PR   25-AUG-2000; 2000US-00648215.
XX
PA   (FISH/) FISHER C.
PA   (HEWW/) HE W.
XX
PI   Fisher C,  He W;
XX
DR   WPI; 2001-647983/74.
XX
PT   Identifying E7-induced cyclin-dependent kinase-2 activity inhibitor,
PT   comprises identifying test compounds which reduce cyclin-dependent kinase
PT   -2 substrate phosphorylation in presence of human papillomavirus E7 or
PT   its fragment.
XX
PS   Claim 1; Page 12-13; 21pp; English.
XX
CC   The invention relates to identifying inhibitor of E7-induced cyclin-
CC   dependent kinase-2 (CDK2) kinase (I) activity, comprising measuring (I)
CC   activity on CDK2 substrate in the presence of human papillomavirus (HPV)
CC   E7 or its fragment, and in the presence and absence of test compound. The
CC   test compound is identified as inhibitor of E7-induced (I) activity when
CC   decreased phosphorylation of CDK2 substrate is detected. The method is
CC   used for identifying inhibitor of E7-induced CDK2 kinase activity. This
CC   method is useful for identifying an antiviral agent which involves
CC   identifying an inhibitor of E7-induced increase in CDK2 kinase activity,
CC   measuring viral proliferation in the presence and absence of identified
CC   inhibitor and identifying the inhibitor as an antiviral agent when
CC   decreased proliferation is detected, in the presence of the inhibitor
CC   compared to viral proliferation in the absence of the inhibitor. The
CC   identified inhibitors are useful for reducing HPV E7-induced kinase
CC   activity or for ameliorating HPV proliferation by inhibiting E7-induced
CC   proliferation in a HPV infected cell by inhibiting E7-binding to CDK2
CC   kinase complex. The inhibitors identified by the above method are useful
CC   for produced medicament for ameliorating viral infection e.g. HPV
CC   infection, adenoviral infection or simian virus 40 (SV40) infection. The
```

CC present sequence represents the amino acid sequence of HPV E7 fragment as
CC described in the method of the invention. (Updated on 06-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 98 AA;

Query Match 100.0%; Score 105; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80
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Search completed: January 5, 2005, 11:16:31
Job time : 157 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 5, 2005, 11:07:41 ; Search time 189 Seconds
(without alignments)
60.886 Million cell updates/sec

Title: US-10-827-083-4
Perfect score: 105
Sequence: 1 CDSTLRLCVQSTHVDIRTLE 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	105	100.0	93	2	Q9QDH2	Q9qdh2 human papil
2	105	100.0	93	2	Q9QDH4	Q9qdh4 human papil
3	105	100.0	93	2	Q9QDH6	Q9qdh6 human papil
4	105	100.0	93	2	Q9QDH8	Q9qdh8 human papil
5	105	100.0	94	2	Q8B5P6	Q8b5p6 human papil
6	105	100.0	98	1	VE7_HPV16	P03129 human papil
7	105	100.0	98	2	O11650	O11650 human papil
8	105	100.0	98	2	O12337	O12337 human papil
9	105	100.0	98	2	Q778H3	Q778h3 human papil
10	105	100.0	98	2	Q778H5	Q778h5 human papil
11	105	100.0	98	2	Q8QRD2	Q8qrd2 human papil
12	105	100.0	98	2	Q8QRD3	Q8qrd3 human papil
13	105	100.0	98	2	CAB45382	Cab45382 human pap
14	105	100.0	98	2	CAB45105	Cab45105 human pap
15	105	100.0	98	2	CAB45107	Cab45107 human pap
16	105	100.0	98	2	CAB45109	Cab45109 human pap
17	105	100.0	98	2	CAB45111	Cab45111 human pap
18	105	100.0	98	2	CAB45113	Cab45113 human pap
19	105	100.0	98	2	CAB45115	Cab45115 human pap
20	105	100.0	98	2	CAB45121	Cab45121 human pap
21	105	100.0	98	2	CAB45123	Cab45123 human pap
22	105	100.0	98	2	CAB45125	Cab45125 human pap
23	105	100.0	98	2	CAB45127	Cab45127 human pap
24	105	100.0	98	2	CAB45129	Cab45129 human pap
25	105	100.0	98	2	CAB45131	Cab45131 human pap
26	105	100.0	98	2	AAD33253	Aad33253 human pap
27	105	100.0	98	2	AAL96633	Aal96633 human pap
28	105	100.0	98	2	AAL96640	Aal96640 human pap
29	105	100.0	98	2	AAL96642	Aal96642 human pap
30	105	100.0	98	2	AAL96644	Aal96644 human pap
31	105	100.0	98	2	AAL96645	Aal96645 human pap
32	105	100.0	98	2	AAL96646	Aal96646 human pap
33	105	100.0	98	2	AAL96647	Aal96647 human pap
34	105	100.0	98	2	AAL96648	Aal96648 human pap
35	105	100.0	98	2	AAL96652	Aal96652 human pap
36	105	100.0	98	2	AAL96653	Aal96653 human pap
37	105	100.0	98	2	AAL96654	Aal96654 human pap
38	105	100.0	98	2	AAL96657	Aal96657 human pap
39	105	100.0	98	2	AAM74160	Aam74160 human pap
40	105	100.0	98	2	AAM11876	Aam11876 human pap
41	105	100.0	98	2	AAM11878	Aam11878 human pap
42	105	100.0	98	2	AAM11880	Aam11880 human pap
43	105	100.0	98	2	AAM11882	Aam11882 human pap
44	105	100.0	98	2	AAM11884	Aam11884 human pap
45	105	100.0	98	2	AAO15698	Aao15698 human pap

ALIGNMENTS

RESULT 1
Q9QDH2
ID Q9QDH2 PRELIMINARY; PRT; 93 AA.
AC Q9QDH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF187869; AAF13399.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 93 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 105; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRLCVQSTHVDIRTLE 20
||||||||||||||||||||
Db 61 CDSTLRLCVQSTHVDIRTLE 80

RESULT 2
Q9QDH4
ID Q9QDH4 PRELIMINARY; PRT; 93 AA.
AC Q9QDH4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF187868; AAF13397.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 93 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 105; DB 2; Length 93;

```
 Best Local Similarity   100.0%;  Pred. No. 1.5e-09;
 Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 3
Q9QDH6
ID   Q9QDH6       PRELIMINARY;      PRT;    93 AA.
AC   Q9QDH6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   E7 protein (Fragment).
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF187867; AAF13395.1; -.
DR   InterPro; IPR000148; Papvi_E7.
DR   Pfam; PF00527; E7; 1.
FT   NON_TER      93      93
SQ   SEQUENCE   93 AA;  10513 MW;  92C7054341326A1F CRC64;

  Query Match             100.0%;  Score 105;  DB 2;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 4
Q9QDH8
ID   Q9QDH8       PRELIMINARY;      PRT;    93 AA.
AC   Q9QDH8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   E7 protein (Fragment).
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF187866; AAF13393.1; -.
DR   InterPro; IPR000148; Papvi_E7.
DR   Pfam; PF00527; E7; 1.
FT   NON_TER      93      93
SQ   SEQUENCE   93 AA;  10452 MW;  83281BB2AE2C8A1F CRC64;

  Query Match             100.0%;  Score 105;  DB 2;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 5
Q8B5P6
ID   Q8B5P6       PRELIMINARY;      PRT;    94 AA.
AC   Q8B5P6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   E7 oncoprotein (Fragment).
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ponglikitmongkol M., Vaeteewoottacharn K.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF469197; AAO15692.1; -.
DR   InterPro; IPR000148; Papvi_E7.
DR   Pfam; PF00527; E7; 1.
FT   NON_TER      94      94
SQ   SEQUENCE   94 AA;  10555 MW;  7CC3281BB2AE2C8A CRC64;

  Query Match             100.0%;  Score 105;  DB 2;  Length 94;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 6
VE7_HPV16
ID   VE7_HPV16       STANDARD;      PRT;    98 AA.
AC   P03129;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   E7 protein.
GN   Name=E7;
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85246220; PubMed=2990099;
RA   Seedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G.;
RT   "Human papillomavirus type 16 DNA sequence.";
RL   Virology 145:181-185(1985).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90218027; PubMed=2157796;
RA   Schneider-Maunoury S., Pehau-Arnaudet G., Breitburd F., Orth G.;
RT   "Expression of the human papillomavirus type 16 genome in SK-v cells,
RT   a line derived from a vulvar intraepithelial neoplasia.";
RL   J. Gen. Virol. 71:809-817(1990).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA   Beth-Giraldo E., Giraldo G.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   FUNCTION.
RX   MEDLINE=88223347; PubMed=2836062;
RA   Phelps W.C., Yee C.L., Munger K., Howley P.M.;
RT   "The human papillomavirus type 16 E7 gene encodes transactivation and
RT   transformation functions similar to those of adenovirus E1A.";
RL   Cell 53:539-547(1988).
CC   -!- FUNCTION: E7 protein has both transforming and trans-activating
CC       activities.
CC   -!- SIMILARITY: LOCAL WITH ADENOVIRUS E1A AND SV40 LT.
```

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CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; K02718; AAA46940.1; -.
DR   EMBL; D00735; BAA00633.1; -.
DR   EMBL; U76411; AAB18962.1; -.
DR   EMBL; U76412; AAB18963.1; -.
DR   EMBL; U76413; AAB18964.1; -.
DR   EMBL; AF003020; AAB70737.1; -.
DR   EMBL; AF003023; AAB70740.1; -.
DR   EMBL; AF003024; AAB70741.1; -.
DR   EMBL; AF003025; AAB70742.1; -.
DR   EMBL; AF003026; AAB70743.1; -.
DR   PIR; A03688; W7WLHS.
DR   InterPro; IPR000148; Papvi_E7.
DR   Pfam; PF00527; E7; 1.
KW   DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW   Transcription regulation.
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FT   SITE         91     94       C-XX-C motif-2.
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Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 7
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ID   O11650      PRELIMINARY;      PRT;    98 AA.
AC   O11650;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Putative transforming protein E7.
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97407827; PubMed=9264576;
RA   Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
RA   Lee H.P.;
RT   "Major sequence variants in E7 gene of human papillomavirus type 16
RT   from cervical cancerous and noncancerous lesions of Korean women.";
RL   Gynecol. Oncol. 66:275-281(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
RA   Lee H.-P.;
RL   Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Terai M., Ma Z., Burk R.D.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22182962; PubMed=12195358;
RA   Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA   Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT   "Human papillomavirus type 16 intratypic variant infection and risk
RT   for cervical neoplasia in southern China.";
RL   J. Infect. Dis. 186:696-700(2002).
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Terai M., Fu L., Ma Z., Burk R.D.;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U76404; AAC58243.1; -.
DR   EMBL; AF472509; AAO15706.1; -.
DR   EMBL; AF486326; AAL96631.1; -.
DR   EMBL; AF486327; AAL96632.1; -.
DR   EMBL; AF486330; AAL96635.1; -.
DR   EMBL; AF486331; AAL96636.1; -.
DR   EMBL; AF486332; AAL96637.1; -.
DR   EMBL; AF486333; AAL96638.1; -.
DR   EMBL; AF486334; AAL96639.1; -.
DR   EMBL; AF486336; AAL96641.1; -.
DR   EMBL; AF486338; AAL96643.1; -.
DR   EMBL; AF486346; AAL96651.1; -.
DR   EMBL; AF486350; AAL96655.1; -.
DR   EMBL; AF486351; AAL96656.1; -.
DR   EMBL; AF534061; AAQ10404.1; -.
DR   InterPro; IPR000148; Papvi_E7.
DR   Pfam; PF00527; E7; 1.
SQ   SEQUENCE   98 AA;  10995 MW;  81E53B534CC3281B CRC64;

  Query Match             100.0%;  Score 105;  DB 2;  Length 98;
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
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Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 8
O12337
ID   O12337      PRELIMINARY;      PRT;    98 AA.
AC   O12337;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   E7 protein.
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97437474; PubMed=9292007;
RA   Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA   Beth-Giraldo E., Giraldo G.;
RT   "Sequence variations and viral genomic state of human papillomavirus
RT   type 16 in penile carcinomas from Ugandan patients.";
RL   J. Gen. Virol. 78:2199-2208(1997).
DR   EMBL; AF003021; AAB70738.1; -.
DR   InterPro; IPR000148; Papvi_E7.
DR   Pfam; PF00527; E7; 1.
SQ   SEQUENCE   98 AA;  11056 MW;  19DEB8F14CD2C705 CRC64;

  Query Match             100.0%;  Score 105;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
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Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 9
Q778H3
ID   Q778H3      PRELIMINARY;      PRT;    98 AA.
AC   Q778H3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   E7 protein (Fragment).
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20112892; PubMed=10644829;
RA   van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA   Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT   "Analysis of human papillomavirus type 16 E6 variants in relation to
RT   p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL   J. Gen. Virol. 81:317-325(2000).
DR   EMBL; AJ388063; CAB45119.1; -.
DR   InterPro; IPR000148; Papvi_E7.
DR   Pfam; PF00527; E7; 1.
FT   NON_TER      98      98
SQ   SEQUENCE   98 AA;  10995 MW;  81E53B534CC3281B CRC64;

  Query Match             100.0%;  Score 105;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 10
Q778H5
ID   Q778H5      PRELIMINARY;      PRT;    98 AA.
AC   Q778H5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   E7 protein (Fragment).
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20112892; PubMed=10644829;
RA   van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA   Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT   "Analysis of human papillomavirus type 16 E6 variants in relation to
RT   p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL   J. Gen. Virol. 81:317-325(2000).
DR   EMBL; AJ388062; CAB45117.1; -.
DR   InterPro; IPR000148; Papvi_E7.
DR   Pfam; PF00527; E7; 1.
FT   NON_TER      98      98
SQ   SEQUENCE   98 AA;  10995 MW;  81E53B534CC3281B CRC64;

  Query Match             100.0%;  Score 105;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-09;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 11
Q8QRD2
ID   Q8QRD2      PRELIMINARY;      PRT;    98 AA.
AC   Q8QRD2;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   E7 protein.
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22182962; PubMed=12195358;
RA   Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA   Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT   "Human papillomavirus type 16 intratypic variant infection and risk
RT   for cervical neoplasia in southern China.";
RL   J. Infect. Dis. 186:696-700(2002).
DR   EMBL; AF486345; AAL96650.1; -.
DR   InterPro; IPR000148; Papvi_E7.
DR   Pfam; PF00527; E7; 1.
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Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 12
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ID   Q8QRD3      PRELIMINARY;      PRT;    98 AA.
AC   Q8QRD3;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   E7 protein.
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC   Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22182962; PubMed=12195358;
RA   Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA   Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT   "Human papillomavirus type 16 intratypic variant infection and risk
RT   for cervical neoplasia in southern China.";
RL   J. Infect. Dis. 186:696-700(2002).
DR   EMBL; AF486344; AAL96649.1; -.
DR   InterPro; IPR000148; Papvi_E7.
DR   Pfam; PF00527; E7; 1.
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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
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Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 13
CAB45382
ID   CAB45382    PRELIMINARY;      PRT;    98 AA.
AC   CAB45382;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   E7 protein (Fragment).
GN   E7.
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
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RC   STRAIN=ET182G;
RA   van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA   Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT   "Analysis of Human papillomavirus type 16 E6 variants in relation to
RT   p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL   J. Gen. Virol. 81:317-325(2000).
DR   EMBL; AJ242681; CAB45382.1; -.
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Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 14
CAB45105
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AC   CAB45105;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   E7 protein (Fragment).
GN   E7.
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=EA7768T;
RA   van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA   Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT   "Analysis of Human papillomavirus type 16 E6 variants in relation to
RT   p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL   J. Gen. Virol. 81:317-325(2000).
DR   EMBL; AJ388056; CAB45105.1; -.
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SQ   SEQUENCE   98 AA;  11022 MW;  9BD612534CD2C9EB CRC64;

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
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Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 15
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ID   CAB45107    PRELIMINARY;      PRT;    98 AA.
AC   CAB45107;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   E7 protein (Fragment).
GN   E7.
OS   Human papillomavirus type 16.
OC   Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
OX   NCBI_TaxID=10581;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=EG169G;
RA   van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA   Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT   "Analysis of Human papillomavirus type 16 E6 variants in relation to
RT   p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL   J. Gen. Virol. 81:317-325(2000).
DR   EMBL; AJ388057; CAB45107.1; -.
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SQ   SEQUENCE   98 AA;  11022 MW;  9BD612534CD2C9EB CRC64;

  Query Match             100.0%;  Score 105;  DB 2;  Length 98;
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Qy          1 CDSTLRLCVQSTHVDIRTLE 20
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Db         61 CDSTLRLCVQSTHVDIRTLE 80


Search completed: January  5, 2005, 11:19:45
Job time : 189 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 5, 2005, 11:19:53 ; Search time 141 Seconds
(without alignments)
51.025 Million cell updates/sec

Title: US-10-827-083-4
Perfect score: 105
Sequence: 1 CDSTLRLCVQSTHVDIRTLE 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	105	100.0	20	10	US-09-828-645-4	Sequence 4, Appli
2	105	100.0	98	9	US-09-728-466-1	Sequence 1, Appli
3	105	100.0	98	9	US-09-820-765-4	Sequence 4, Appli
4	105	100.0	98	9	US-09-824-017-4	Sequence 4, Appli
5	105	100.0	98	10	US-09-986-118A-4	Sequence 4, Appli
6	105	100.0	98	14	US-10-267-311-8	Sequence 8, Appli
7	105	100.0	98	14	US-10-177-390-8	Sequence 8, Appli
8	105	100.0	98	14	US-10-201-764-19	Sequence 19, Appl
9	105	100.0	98	15	US-10-654-129-4	Sequence 4, Appli
10	105	100.0	98	15	US-10-681-410-19	Sequence 19, Appl
11	105	100.0	98	16	US-10-772-988-3	Sequence 3, Appli
12	105	100.0	98	16	US-10-479-541-5	Sequence 5, Appli
13	105	100.0	99	15	US-10-115-440-7	Sequence 7, Appli
14	105	100.0	111	16	US-10-472-724-4	Sequence 4, Appli
15	105	100.0	121	14	US-10-267-311-12	Sequence 12, Appl
16	105	100.0	198	14	US-10-267-311-35	Sequence 35, Appl
17	105	100.0	220	13	US-10-000-903-1	Sequence 1, Appli
18	105	100.0	220	13	US-10-000-903-8	Sequence 8, Appli
19	105	100.0	239	13	US-10-000-903-12	Sequence 12, Appl
20	105	100.0	266	9	US-09-367-309A-1	Sequence 1, Appli
21	105	100.0	289	15	US-10-115-440-5	Sequence 5, Appli
22	105	100.0	295	14	US-10-267-311-33	Sequence 33, Appl
23	105	100.0	324	14	US-10-267-311-25	Sequence 25, Appl
24	105	100.0	334	16	US-10-472-724-10	Sequence 10, Appl
25	105	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
26	105	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
27	105	100.0	421	14	US-10-296-770-7	Sequence 7, Appli
28	105	100.0	493	14	US-10-267-311-19	Sequence 19, Appl
29	105	100.0	639	14	US-10-267-311-17	Sequence 17, Appl
30	105	100.0	641	14	US-10-267-311-51	Sequence 51, Appl
31	105	100.0	647	14	US-10-267-311-53	Sequence 53, Appl
32	105	100.0	648	14	US-10-267-311-29	Sequence 29, Appl
33	105	100.0	711	14	US-10-267-311-41	Sequence 41, Appl
34	105	100.0	724	14	US-10-267-311-45	Sequence 45, Appl
35	105	100.0	805	14	US-10-367-095-9	Sequence 9, Appli
36	105	100.0	805	15	US-10-368-046-9	Sequence 9, Appli
37	105	100.0	805	16	US-10-367-367-9	Sequence 9, Appli
38	97	92.4	98	14	US-10-392-113-29	Sequence 29, Appl
39	96	91.4	19	16	US-10-479-541-1	Sequence 1, Appli
40	91	86.7	18	14	US-10-355-268-16	Sequence 16, Appl
41	85	81.0	20	10	US-09-828-645-8	Sequence 8, Appli
42	83.5	79.5	19	9	US-09-888-721-7	Sequence 7, Appli
43	83.5	79.5	19	15	US-10-668-400-9	Sequence 9, Appli
44	82	78.1	15	16	US-10-306-541-89	Sequence 89, Appl
45	82	78.1	20	15	US-10-432-465-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1
US-09-828-645-4
; Sequence 4, Application US/09828645
; Publication No. US20030027750A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yao Xiong
; TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus
; FILE REFERENCE: 146-1-002
; CURRENT APPLICATION NUMBER: US/09/828,645
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/194,796
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E7 early region of HPV-16
US-09-828-645-4

Query Match 100.0%; Score 105; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRLCVQSTHVDIRTLE 20
||||||||||||||||||||
Db 1 CDSTLRLCVQSTHVDIRTLE 20

RESULT 2
US-09-728-466-1
; Sequence 1, Application US/09728466
; Patent No. US20010029022A1
; GENERAL INFORMATION:

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;  APPLICANT:  Fisher, Christopher
;  APPLICANT:  He, Wanxia
;  TITLE OF INVENTION:  Methods to Identify Anti-Viral Agents
;  FILE REFERENCE:  28341/6216
;  CURRENT APPLICATION NUMBER: US/09/728,466
;  CURRENT FILING DATE:  2000-12-01
;  PRIOR APPLICATION NUMBER:  09/382,616
;  PRIOR FILING DATE:  1999-08-25
;  NUMBER OF SEQ ID NOS:  43
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;    LENGTH: 98
;    TYPE: PRT
;    ORGANISM: Papillomavirus sylvilagi
US-09-728-466-1

  Query Match             100.0%;  Score 105;  DB 9;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 3
US-09-820-765-4
; Sequence 4, Application US/09820765
; Publication No. US20020039584A1
;   GENERAL INFORMATION:
;        APPLICANT: BURGER, Alexander
;                   HALLEK, Michael
;        TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
;                            FORMULATIONS AND METHODS OF USE
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FOLEY & LARDNER
;             STREET: 3000 K Street, N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/820,765
;             FILING DATE: 30-Mar-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 09/026,896
;             FILING DATE: 20-FEB-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sandercock, Colin G.
;             REGISTRATION NUMBER: 31,298
;             REFERENCE/DOCKET NUMBER: 37067/102
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 672-5300
;             TELEFAX: (202) 672-5399
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 98 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-765-4

  Query Match             100.0%;  Score 105;  DB 9;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 4
US-09-824-017-4
; Sequence 4, Application US/09824017
; Publication No. US20020197668A1
;   GENERAL INFORMATION:
;        APPLICANT: BURGER, Alexander
;                   HALLEK, Michael
;        TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
;                            FORMULATIONS AND METHODS OF USE
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FOLEY & LARDNER
;             STREET: 3000 K Street, N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/824,017
;             FILING DATE: 03-Apr-2001
;             CLASSIFICATION: 424
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/026,896
;             FILING DATE: 1998-02-20
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sandercock, Colin G.
;             REGISTRATION NUMBER: 31,298
;             REFERENCE/DOCKET NUMBER: 37067/102
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 672-5300
;             TELEFAX: (202) 672-5399
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 98 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-824-017-4

  Query Match             100.0%;  Score 105;  DB 9;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 5
US-09-986-118A-4
; Sequence 4, Application US/09986118A
; Publication No. US20030021806A1
;   GENERAL INFORMATION:
;        APPLICANT: BURGER, Alexander
;                   HALLEK, Michael
;        TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
;                            FORMULATIONS AND METHODS OF USE
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FOLEY & LARDNER
;             STREET: 3000 K Street, N.W.
;
```

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;              CITY: Washington
;              STATE: D.C.
;              COUNTRY: U.S.A.
;              ZIP: 20007-5109
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/986,118A
;              FILING DATE: 07-No. US20030021806A1-2001
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US 09/026,896
;              FILING DATE: <Unknown>
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Sandercock, Colin G.
;              REGISTRATION NUMBER: 31,298
;              REFERENCE/DOCKET NUMBER: 37067/102
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (202) 672-5300
;              TELEFAX: (202) 672-5399
;    INFORMATION FOR SEQ ID NO: 4:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 98 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-986-118A-4

  Query Match             100.0%;  Score 105;  DB 10;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 6
US-10-267-311-8
; Sequence 8, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Marvin
;  APPLICANT:  Chu, N. Randall
;  APPLICANT:  Mizzen, Lee A.
;  TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
;  FILE REFERENCE: 12071/002001
;  CURRENT APPLICATION NUMBER: US/10/267,311
;  CURRENT FILING DATE:  2002-10-09
;  PRIOR APPLICATION NUMBER: US/09/613,303
;  PRIOR FILING DATE: 2000-07-10
;  PRIOR APPLICATION NUMBER: US 60/143,757
;  PRIOR FILING DATE: 1999-07-08
;  NUMBER OF SEQ ID NOS: 55
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: fusion sequence
US-10-267-311-8

  Query Match             100.0%;  Score 105;  DB 14;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 7
US-10-177-390-8
; Sequence 8, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
;  APPLICANT: Schuler, Gerold
;  APPLICANT:  N.V. Antwerps Innovatiecentrum
;  TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
;  TITLE OF INVENTION:  Polynucleotides by Electroporation
;  FILE REFERENCE: 021505wo/JH/ml
;  CURRENT APPLICATION NUMBER: US/10/177,390
;  CURRENT FILING DATE:  2002-06-20
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: fragment of
;   OTHER INFORMATION: human papilloma virus type 16 E7 gene
US-10-177-390-8

  Query Match             100.0%;  Score 105;  DB 14;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 8
US-10-201-764-19
; Sequence 19, Application US/10201764
; Publication No. US20030166140A1
; GENERAL INFORMATION:
;  APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
;  TITLE OF INVENTION:  IMMUNE RESPONSE
;  FILE REFERENCE: TBA
;  CURRENT APPLICATION NUMBER: US/10/201,764
;  CURRENT FILING DATE:  2002-07-22
;  PRIOR APPLICATION NUMBER: US/09/566,420
;  PRIOR FILING DATE: 2000-05-05
;  PRIOR APPLICATION NUMBER: 60/132,752
;  PRIOR FILING DATE: 1999-05-06
;  PRIOR APPLICATION NUMBER: 60/132,750
;  PRIOR FILING DATE: 1999-05-06
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Human papillomavirus type E7
US-10-201-764-19

  Query Match             100.0%;  Score 105;  DB 14;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 9
US-10-654-129-4
; Sequence 4, Application US/10654129
; Publication No. US20040081661A1
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;   GENERAL INFORMATION:
;        APPLICANT: BURGER, Alexander
;                   HALLEK, Michael
;        TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
;                            FORMULATIONS AND METHODS OF USE
;        NUMBER OF SEQUENCES: 28
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FOLEY & LARDNER
;             STREET: 3000 K Street, N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/654,129
;             FILING DATE: 04-Sep-2003
;             CLASSIFICATION: 424
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/824,017
;             FILING DATE: 03-Apr-2001
;             APPLICATION NUMBER: 09/026,896
;             FILING DATE: 1998-02-20
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sandercock, Colin G.
;             REGISTRATION NUMBER: 31,298
;             REFERENCE/DOCKET NUMBER: 37067/102
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 672-5300
;             TELEFAX: (202) 672-5399
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 98 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-654-129-4

  Query Match             100.0%;  Score 105;  DB 15;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 10
US-10-681-410-19
; Sequence 19, Application US/10681410
; Publication No. US20040096426A1
; GENERAL INFORMATION:
;  APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
;  TITLE OF INVENTION:  IMMUNE RESPONSE
;  FILE REFERENCE: TBA
;  CURRENT APPLICATION NUMBER: US/10/681,410
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: US/10/201,764
;  PRIOR FILING DATE: 2002-07-22
;  PRIOR APPLICATION NUMBER: US/09/566,420
;  PRIOR FILING DATE: 2000-05-05
;  PRIOR APPLICATION NUMBER: 60/132,752
;  PRIOR FILING DATE: 1999-05-06
;  PRIOR APPLICATION NUMBER: 60/132,750
;  PRIOR FILING DATE: 1999-05-06
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Human papillomavirus type E7
US-10-681-410-19

  Query Match             100.0%;  Score 105;  DB 15;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 11
US-10-772-988-3
; Sequence 3, Application US/10772988
; Publication No. US20040139485A1
; GENERAL INFORMATION:
;  APPLICANT: Thorgeirsson, Snorri S.
;  APPLICANT:  Woitach, Joseph T.
;  APPLICANT:  Zhang, Minghuang
;  TITLE OF INVENTION: cDNA ENCODING A GENE BOG (B5T OVER-EXPRESSED GENE) AND ITS PROTEI
;  TITLE OF INVENTION:  PRODUCT
;  FILE REFERENCE: 11613.29USW1
;  CURRENT APPLICATION NUMBER: US/10/772,988
;  CURRENT FILING DATE:  2004-02-05
;  PRIOR APPLICATION NUMBER: US/09/637,746
;  PRIOR FILING DATE: 2000-08-11
;  PRIOR APPLICATION NUMBER: PCT/US99/04142
;  PRIOR FILING DATE: 1999-02-25
;  PRIOR APPLICATION NUMBER: US 60/079,567
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: US 60/075,922
;  PRIOR FILING DATE: 1998-02-25
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Human papillomavirus
US-10-772-988-3

  Query Match             100.0%;  Score 105;  DB 16;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 1e-08;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80


RESULT 12
US-10-479-541-5
; Sequence 5, Application US/10479541
; Publication No. US20040151723A1
; GENERAL INFORMATION:
;  APPLICANT: Kirin Beer Kabushiki Kaisha
;  TITLE OF INVENTION: Novel E7 antigen epitope from human papillomavirus and
;  TITLE OF INVENTION:  CD4+ T cells activated thereby
;  FILE REFERENCE: 137240PX
;  CURRENT APPLICATION NUMBER: US/10/479,541
;  CURRENT FILING DATE:  2003-12-04
;  PRIOR APPLICATION NUMBER: 173803/2001
;  PRIOR FILING DATE: 2001-06-08
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Human papillomavirus type 16
US-10-479-541-5
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Query Match 100.0%; Score 105; DB 16; Length 98;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRLCVQSTHVDIRTLE 20
||||||||||||||||||||
Db 61 CDSTLRLCVQSTHVDIRTLE 80

RESULT 13
US-10-115-440-7
; Sequence 7, Application US/10115440
; Publication No. US20040086845A1
; GENERAL INFORMATION:
; APPLICANT: WU, Tzyy-Choou
; APPLICANT: HUNG, Chien-Fu
; TITLE OF INVENTION: SUPERIOR MOLECULAR VACCINE LINKING THE TRANSLOCATION DOMAIN OF A
; TITLE OF INVENTION: BACTERIAL TOXIN TO AN ANTIGEN
; FILE REFERENCE: 02240-179934
; CURRENT APPLICATION NUMBER: US/10/115,440
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 60/281,003
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: PCT/US00/41422
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 09/501,097
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/421,608
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-115-440-7

Query Match 100.0%; Score 105; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRLCVQSTHVDIRTLE 20
||||||||||||||||||||
Db 61 CDSTLRLCVQSTHVDIRTLE 80

RESULT 14
US-10-472-724-4
; Sequence 4, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-4

Query Match 100.0%; Score 105; DB 16; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRLCVQSTHVDIRTLE 20
||||||||||||||||||||
Db 66 CDSTLRLCVQSTHVDIRTLE 85

RESULT 15
US-10-267-311-12
; Sequence 12, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-12

Query Match 100.0%; Score 105; DB 14; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CDSTLRLCVQSTHVDIRTLE 20
||||||||||||||||||||
Db 84 CDSTLRLCVQSTHVDIRTLE 103

Search completed: January 5, 2005, 11:32:03
Job time : 141 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 5, 2005, 11:10:56 ; Search time 38 Seconds
(without alignments)
50.640 Million cell updates/sec

Title: US-10-827-083-4
Perfect score: 105
Sequence: 1 CDSTLRLCVQSTHVDIRTLE 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	105	100.0	98	1	W7WLHS	E7 protein - human
2	91	86.7	99	1	W7WL35	E7 protein - human
3	81	77.1	98	1	W7WL31	E7 protein - human
4	80	76.2	99	2	S36574	E7 protein - human
5	68	64.8	98	1	W7WL58	E7 protein - human
6	66	62.9	97	1	W7WL33	E7 protein - human
7	58	55.2	98	1	W7WL6	E7 protein - human
8	56	53.3	86	2	S36533	E7 protein - human
9	56	53.3	97	2	S36516	E7 protein - human
10	54	51.4	98	1	W7WL11	E7 protein - human
11	51	48.6	95	2	S36480	E7 protein - human
12	50	47.6	106	2	S36562	E7 protein - human
13	50	47.6	113	1	W7WLR1	E7 protein - rhesu
14	49	46.7	92	1	S15622	E7 protein - human
15	49	46.7	104	2	S36545	E7 protein - human
16	47	44.8	93	1	W7WL42	E7 protein - human
17	46	43.8	103	2	S36539	E7 protein - human
18	45	42.9	92	1	S15615	E7 protein - human
19	45	42.9	98	1	W7WLC1	E7 protein - pygmy
20	45	42.9	102	2	S36492	E7 protein - human
21	44	41.9	93	2	S36474	E7 protein - human
22	44	41.9	105	2	S36528	E7 protein - human
23	43	41.0	102	2	S36486	E7 protein - human
24	42	40.0	93	1	W7WL	E7 protein - human
25	42	40.0	102	1	W7WLEP	E7 protein - Europ
26	42	40.0	251	2	H84861	3-isopropylmalate
27	42	40.0	267	1	DCBYOF	orotidine-5'-phosp
28	42	40.0	267	1	DEBYOP	orotidine-5'-phosp
29	42	40.0	338	2	T26113	hypothetical prote
30	42	40.0	449	2	T19554	hypothetical prote
31	42	40.0	1966	2	T08991	hypothetical prote
32	41.5	39.5	349	2	I38904	TATA-binding prote
33	41.5	39.5	360	2	T19024	hypothetical prote
34	41	39.0	92	2	A82141	integration host f
35	41	39.0	231	2	S26035	cytochrome-c oxida
36	41	39.0	394	2	E90115	26S protease regul
37	41	39.0	395	2	E90546	phosphopentomutase
38	41	39.0	396	2	H87356	hypothetical prote
39	41	39.0	405	2	T40193	hypothetical prote
40	41	39.0	458	2	G81379	ferredoxin domain-
41	41	39.0	577	2	H72739	probable molybdopt
42	41	39.0	1213	2	A41724	limb deformity (ld
43	41	39.0	1250	2	T40062	probable nuclear e
44	41	39.0	1401	2	S11527	alpha-latrotoxin p
45	40	38.1	103	1	W7WL47	E7 protein - human

ALIGNMENTS

RESULT 1
W7WLHS
E7 protein - human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03688; S12367; T10428
R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
A;Accession: A03688
A;Molecule type: DNA
A;Residues: 1-98 <SEE>
A;Cross-references: UNIPROT:P03129; GB:K02718; NID:g333031; PIDN:AAA46940.1; PID:g33303
R;Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H.
EMBO J. 9, 153-160, 1990
A;Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 lar
A;Reference number: S12367; MUID:90107938; PMID:2153075
A;Accession: S12367
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-98 <BAR>
R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A;Title: A negative element in the human poapillomavirus type 16 genome acts at the lev
A;Reference number: Z17014; MUID:91162763; PMID:1848319
A;Accession: T10428
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-98 <KEN>
A;Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033
C;Genetics:
A;Gene: E7
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;58-94/Region: zinc finger CCCC motif

Query Match 100.0%; Score 105; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||||||||||||||
Db         61 CDSTLRLCVQSTHVDIRTLE 80
```

RESULT 2
W7WL35
E7 protein - human papillomavirus type 35
C;Species: human papillomavirus type 35
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

```
C;Accession: F40824; S36522
R;Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A;Title: The phylogenetic relationship and complete nucleotide sequence of human papillo
A;Reference number: A40824; MUID:92124753; PMID:1310198
A;Accession: F40824
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-99 <MAR>
A;Cross-references: UNIPROT:P27230; GB:M74117; NID:g333050; PIDN:AAA46967.1; PID:g333052
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36522
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <DEL>
A;Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52562.1; PID:g396999
A;Experimental source: strain 35H
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;59-95/Region: zinc finger CCCC motif

  Query Match             86.7%;  Score 91;  DB 1;  Length 99;
  Best Local Similarity   80.0%;  Pred. No. 4.8e-08;
  Matches   16;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              |::|||||||||:||| ||
Db         62 CEATLRLCVQSTHIDIRKLE 81


RESULT 3
W7WL31
E7 protein - human papillomavirus type 31
C;Species: human papillomavirus type 31
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: B32444
R;Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-assoc
A;Reference number: A94398; MUID:89299478; PMID:2545036
A;Accession: B32444
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <GOL>
A;Cross-references: UNIPROT:P17387; GB:J04353; NID:g333048; PIDN:AAA46951.1; PID:g459917
C;Comment: This protein may be involved in the oncogenic potential of this virus.
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;58-94/Region: zinc finger CCCC motif

  Query Match             77.1%;  Score 81;  DB 1;  Length 98;
  Best Local Similarity   80.0%;  Pred. No. 2.3e-06;
  Matches   16;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              | |||||||||| |||| |:
Db         61 CKSTLRLCVQSTQVDIRILQ 80


RESULT 4
S36574
E7 protein - human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 08-May-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S36574
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36574
A;Molecule type: DNA
A;Residues: 1-99 <DEL>
A;Cross-references: UNIPROT:P36831; EMBL:X74481; NID:g397038; PIDN:CAA52586.1; PID:g3970
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation

  Query Match             76.2%;  Score 80;  DB 2;  Length 99;
  Best Local Similarity   70.0%;  Pred. No. 3.4e-06;
  Matches   14;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||||||||: ||  |:|||:
Db         63 CDSTLRLCIHSTATDLRTLQ 82


RESULT 5
W7WL58
E7 protein - human papillomavirus type 58
C;Species: human papillomavirus type 58
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: F36779
R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A;Title: Human papillomavirus type 58 DNA sequence.
A;Reference number: A36779; MUID:92024102; PMID:1656594
A;Accession: F36779
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <KIR>
A;Cross-references: UNIPROT:P26557; GB:D90400; NID:g222386; PIDN:BAA31846.1; PID:g333705
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;59-95/Region: zinc finger CCCC motif

  Query Match             64.8%;  Score 68;  DB 1;  Length 98;
  Best Local Similarity   55.0%;  Pred. No. 0.00034;
  Matches   11;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              | :|:|||: ||  |:|||:
Db         62 CGTTVRLCINSTTTDVRTLQ 81


RESULT 6
W7WL33
E7 protein - human papillomavirus type 33
C;Species: human papillomavirus type 33
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A03689; S23831; S23827
R;Cole, S.T.; Streeck, R.E.
J. Virol. 58, 991-995, 1986
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 33,
A;Reference number: A93020; MUID:86200464; PMID:3009902
A;Accession: A03689
A;Molecule type: DNA
A;Residues: 1-97 <COL>
A;Cross-references: UNIPROT:P06429; GB:M12732; NID:g333049; PIDN:AAA46959.1; PID:g46317
R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; M
submitted to the EMBL Data Library, January 1992
A;Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via t
A;Reference number: S19906
A;Accession: S23831
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-97 <SNI>
A;Cross-references: EMBL:X64085; NID:g60278; PIDN:CAA45434.1; PID:g60281; EMBL:X64084,
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;58-94/Region: zinc finger CCCC motif

  Query Match             62.9%;  Score 66;  DB 1;  Length 97;
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  Best Local Similarity   55.0%;  Pred. No. 0.00074;
  Matches   11;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              |::|:|||| ||  |:||::
Db         61 CNTTVRLCVNSTASDLRTIQ 80


RESULT 7
W7WL6
E7 protein - human papillomavirus type 6b
C;Species: human papillomavirus type 6b
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: D20558
R;Schwarz, E.; Durst, M.; Demankowski, C.; Lattermann, O.; Zech, R.; Wolfsperger, E.; Su
EMBO J. 2, 2341-2348, 1983
A;Title: DNA sequence and genome organization of genital human papillomavirus type 6b.
A;Reference number: A90975; MUID:84131949; PMID:6321162
A;Accession: D20558
A;Molecule type: DNA
A;Residues: 1-98 <SCH>
A;Cross-references: UNIPROT:P06464; GB:X00203; NID:g60955; PIDN:CAA25019.1; PID:g60957
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;58-94/Region: zinc finger CCCC motif

  Query Match             55.2%;  Score 58;  DB 1;  Length 98;
  Best Local Similarity   55.0%;  Pred. No. 0.016;
  Matches   11;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||| :|| || |  ||| ::
Db         61 CDSNVRLVVQCTETDIREVQ 80


RESULT 8
S36533
E7 protein - human papillomavirus type 10
C;Species: human papillomavirus type 10
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36533
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36533
A;Molecule type: DNA
A;Residues: 1-86 <DEL>
A;Cross-references: UNIPROT:P36818; EMBL:X74465; NID:g396901; PIDN:CAA52490.1; PID:g3969
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation

  Query Match             53.3%;  Score 56;  DB 2;  Length 86;
  Best Local Similarity   55.0%;  Pred. No. 0.031;
  Matches   11;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              |   ||| |: :| ||| ||
Db         52 CSLPLRLVVECSHADIRALE 71


RESULT 9
S36516
E7 protein - human papillomavirus type 34
C;Species: human papillomavirus type 34
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36516
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36516
A;Molecule type: DNA
A;Residues: 1-97 <DEL>
A;Cross-references: UNIPROT:P36828; EMBL:X74476; NID:g396989; PIDN:CAA52556.1; PID:g396
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation

  Query Match             53.3%;  Score 56;  DB 2;  Length 97;
  Best Local Similarity   50.0%;  Pred. No. 0.035;
  Matches   10;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              | ||: | ::||| |:  ||
Db         60 CQSTVCLTIESTHADLLVLE 79


RESULT 10
W7WL11
E7 protein - human papillomavirus type 11
C;Species: human papillomavirus type 11
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
C;Accession: A03690
R;Dartmann, K.; Schwarz, E.; Gissmann, L.; zur Hausen, H.
Virology 151, 124-130, 1986
A;Title: The nucleotide sequence and genome organization of human papilloma virus type
A;Reference number: A94338; MUID:86181601; PMID:3008427
A;Accession: A03690
A;Molecule type: DNA
A;Residues: 1-98 <DAR>
A;Cross-references: UNIPROT:P04020; GB:M14119; NID:g333026; PIDN:AAA46928.1; PID:g49619
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;58-94/Region: zinc finger CCCC motif

  Query Match             51.4%;  Score 54;  DB 1;  Length 98;
  Best Local Similarity   55.0%;  Pred. No. 0.077;
  Matches   11;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||| :|| |: |  ||| |:
Db         61 CDSNVRLVVECTDGDIRQLQ 80


RESULT 11
S36480
E7 protein - human papillomavirus type 17
C;Species: human papillomavirus type 17
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36480
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36480
A;Molecule type: DNA
A;Residues: 1-95 <DEL>
A;Cross-references: UNIPROT:P36821; EMBL:X74469; NID:g396932; PIDN:CAA52513.1; PID:g396
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation

  Query Match             48.6%;  Score 51;  DB 2;  Length 95;
  Best Local Similarity   55.0%;  Pred. No. 0.24;
  Matches   11;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              | | ||| | :||  ||: |
Db         55 CGSKLRLIVLATHAGIRSQE 74


RESULT 12
S36562
E7 protein - human papillomavirus type 45
C;Species: human papillomavirus type 45
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36562
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R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36562
A;Molecule type: DNA
A;Residues: 1-106 <DEL>
A;Cross-references: UNIPROT:P21736; EMBL:X74479; NID:g397022; PIDN:CAA52574.1; PID:g3970
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation

  Query Match             47.6%;  Score 50;  DB 2;  Length 106;
  Best Local Similarity   45.0%;  Pred. No. 0.39;
  Matches    9;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              ||  : | |:|:  |:|||:
Db         69 CDGRIELTVESSAEDLRTLQ 88


RESULT 13
W7WLR1
E7 protein - rhesus papillomavirus (type 1)
C;Species: rhesus papillomavirus
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: B38503
R;Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.
Virology 181, 424-429, 1991
A;Title: Characterization of the complete RhPV 1 genomic sequence and an integration loc
A;Reference number: A38503; MUID:91135018; PMID:1847267
A;Accession: B38503
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-113 <OST>
A;Cross-references: UNIPROT:P22161; EMBL:M37717
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation

  Query Match             47.6%;  Score 50;  DB 1;  Length 113;
  Best Local Similarity   50.0%;  Pred. No. 0.42;
  Matches   10;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              |   ||| | |:| ::| ||
Db         76 CGKPLRLVVVSSHEELRVLE 95


RESULT 14
S15622
E7 protein - human papillomavirus type 57
C;Species: human papillomavirus type 57
A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: S15622
R;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A;Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and
A;Reference number: S15614; MUID:91188699; PMID:1964523
A;Accession: S15622
A;Molecule type: DNA
A;Residues: 1-92 <HIR>
A;Cross-references: UNIPROT:P22160; EMBL:X55965; NID:g60882; PIDN:CAA39431.1; PID:g60884
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;55-91/Region: zinc finger CCCC motif

  Query Match             46.7%;  Score 49;  DB 1;  Length 92;
  Best Local Similarity   55.0%;  Pred. No. 0.5;
  Matches   11;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              | ||:|| |:    ||| ||
Db         58 CHSTVRLVVECGAADIRHLE 77


RESULT 15
S36545
E7 protein - human papillomavirus type 26
C;Species: human papillomavirus type 26
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36545
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36545
A;Molecule type: DNA
A;Residues: 1-104 <DEL>
A;Cross-references: UNIPROT:P36824; EMBL:X74472; NID:g396956; PIDN:CAA52531.1; PID:g396
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation

  Query Match             46.7%;  Score 49;  DB 2;  Length 104;
  Best Local Similarity   45.0%;  Pred. No. 0.56;
  Matches    9;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 CDSTLRLCVQSTHVDIRTLE 20
              |:| ::| |||:  ::| ||
Db         68 CNSIVQLAVQSSRQNVRVLE 87


Search completed: January  5, 2005, 11:20:30
Job time : 39 secs
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